IN THE CLAIM

Please amend claim 1 and add claims 25 through 30 to read as follows.

1. (Currently Amended) A process for quantitating a human DNA in a sample, said 1 process comprising the steps of: 2 providing a sample to be analyzed; 3 amplifying predetermined genomic DNA of an Alu element subfamily by using primers, 4 said Alu element subfamily being more enriched in the human genome than in any non-human 5 primate genome, the amplification being intra-Alu polymerase chain reaction 6 amplification; and 7 measuring the amount of the human DNA by comparing the amplified DNA with a 8 reference to quantitate the human DNA in the sample. 9 2. (Canceled) 1 3. (Canceled) 1 4. (Canceled) 1 The process of claim 1, wherein the amplification is a 5. (Previously Presented) 1

polymerase chain reaction with the primers containing the following sequences:

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3	5' CGAGGCGGTGGATCATGAGGT 3'(SEQ ID NO: 3)
4	and
5	5' TCTGTCGCCCAGGCCGGACT 3' (SEQ ID NO: 4).
1	6. (Previously Presented) The process of claim 1, wherein the amplification is a
2	polymerase chain reaction with the primers containing the following sequences:
3	5' GAGATCGAGACCACGGTGAAA 3' (SEQ ID NO: 5)
4	and
5	5' TTTGAGACGGAGTCTCGTT 3' (SEQ ID NO: 6).
1	7. (Previously Presented) The process of claim 1, wherein the measurement step
2	comprises the step of measuring the amount of the human DNA on an agarose gel stained with
3	ethidium bromide.
1	8. (Previously Presented) The process of claim 1, wherein the measurement step
2	comprises the step of measuring the amount of the human DNA by using a qPCR system.
1	9. (Previously Presented) The process of claim 1, wherein the measurement step
2	comprises the step of measuring the amount of the human DNA by using TaqMan chemistry.
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1	Claims 10-20. (Canceled)

1	21. (Previously Presented) A process for quantitating a human DNA in a sample, said
2	process comprising the steps of:
3	providing a sample to be analyzed;
4	amplifying predetermined genomic DNA containing an Alu element by using primers,
5	said Alu element being present only in the human genome, the amplification being intra-Alu
6	polymerase chain reaction amplification; and
7	measuring the amount of the human DNA by comparing the amplified DNA with a
8	reference.
1	22. (Previously Presented) A process for quantitating a human DNA in a sample, said
2	process comprising the steps of:
3	providing a sample to be analyzed;
4	amplifying predetermined genomic DNA of an Alu element subfamily by using primers,
5	said predetermined genomic DNA including subfamily-specific diagnostic mutations, a copy
6	number of said predetermined genomic DNA in the human genome being higher than a copy
7	number of said predetermined genomic DNA in any non-human primate genome, the
8	amplification being intra-Alu polymerase chain reaction amplification; and
9	measuring the amount of the human DNA by comparing the amplified DNA with a
10	reference.

23. (Previously Presented) The process of claim 1, wherein each of said primers includes 1 a subfamily-specific diagnostic mutation. . 2 24. (Previously Presented) The process of claim 21, wherein each of said primers 1 includes a subfamily-specific diagnostic mutation. 2 25. (New) The process of claim 1, wherein said Alu element subfamily is Yb8 subfamily. 1 26. (New) The process of claim 1, wherein said Alu element subfamily is Ya5 subfamily. 1 27. (New) The process of claim 1, wherein said Alu element subfamily is Yd6 subfamily. 1 The process of claim 22, wherein said Alu element subfamily is Yb8 1 subfamily. 2 The process of claim 22, wherein said Alu element subfamily is Ya5 29. (New) 1 subfamily. 2 The process of claim 22, wherein said Alu element subfamily is Yd6 1 30. (New) 2 subfamily.